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SEQUENCE LISTING

<110> WALLACH, David
BOLDIN, Mark
MALININ, Nikolai

<120> MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH
AND CELL SURVIVAL PATHWAYS

<130> WALLACH24

<140> 01

<141> 1999-12-06

<150> 131011

<151> 1497-06-05

<150> 121199

<151> 1497-06-30

<150> 131746

<151> 1497-03-11

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 540

<212> PFT

<213> Homo sapiens

<200> 1

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
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Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
20 25 30

Arg Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
35 40 45

Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
50 55 60

Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro
65 70 75 80

Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
85 90 95

Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
100 105 110

Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
115 120 125

Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His

130	35	140	
His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val			
145	150	155	160
Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser			
165	170	175	
Gln Ser Arg Ser Ser Lys Ser Ala Pro Gln Gly Gly Thr Ile Ile Tyr			
180	185	190	
Met Pro Pro Gln Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile			
195	200	205	
Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser			
210	215	220	
Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr			
225	230	235	240
Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro			
245	250	255	
Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly			
260	265	270	
Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile			
275	280	285	
Glu Leu Glu Pro Val Leu Arg Thr Phe Gln Glu Ile Thr Phe Leu Glu			
290	295	300	
Ala Val Ile Asn Ile Lys Lys Thr Lys Ile Asn Ser Val Ser Ser Ala			
305	310	315	320
Ile His Ile Cys Asp Lys Lys Met Gln Leu Ser Leu Asn Ile Phe			
325	330	335	
Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His			
340	345	350	
Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln			
355	360	365	
Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys			
370	375	380	
Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly			
385	390	395	400
Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser			
405	410	415	
Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Gln Arg Leu Gln			
420	425	430	
Pro Gly Ile Ala Gln Gln Tp Ile Gln Ser Lys Arg Gln Asp Ile Val			
435	440	445	
Asn Gln Met Thr Gln Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu			
450	455	460	
Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys			

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4

475

480

Pro Thr Arg Thr Ser Lys Val Arg Gln Ile Leu Asp Thr Thr Asp Ile
485 490 495

50

495

13

Ile Gln Glu Phe Ala Lys Val Ile Val Gln Lys Ile Lys Asp Asn
500 505 510

502

509

213

Lys Gin Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
515 520 525

510

E120

520

Ser Pro Ser Leu Asn Leu Leu Glu Asn Lys Ser Met
530 535 540

53

53

5, 4

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1.1.2. cDNA

Homo sapiens

400-2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(B) STREET: BEIT CLOPE, WEIZMANN INSTITUTE OF SCIENCE
(C) CITY: REHOVOT
(E) COUNTRY: ISRAEL
(F) POSTAL CODE (ZIP): 76100

(ii) TITLE OF INVENTION: MODULATORS OF INTRACELLULAR INFLAMMATION,
CELL DEATH AND CELL SURVIVAL PATHWAYS

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 121011
(B) FILING DATE: 05-JUN-1997

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 121199
(B) FILING DATE: 30-JUN-1997

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 121746
(B) FILING DATE: 11-SEP-1997

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
1 5 10 15

Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
20 25 30

Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
35 40 45

Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
50 55 60

Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro
65 70 75 80

Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
85 90 95

Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
100 105 110

Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
115 120 125

Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His
130 135 140

His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
145 150 155 160

Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
165 170 175

Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
180 185 190

Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
195 200 205

Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
210 215 220

Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
225 230 235 240

Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
245 250 255

Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
260 265 270

' Trp Ala Gln Asn P [REDACTED] sp Glu Arg Pro Ser Phe Leu Lys C [REDACTED] Leu Ile
275 280 285

Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
290 295 300

Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
305 310 315 320

Ile His Leu Cys Asp Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
325 330 335

Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
340 345 350

Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
355 360 365

Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
370 375 380

Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
385 390 395 400

Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser
405 410 415

Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
420 425 430

Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
435 440 445

Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
450 455 460

Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
465 470 475 480

Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
485 490 495

Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
500 505 510

Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
515 520 525

Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
530 535 540

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2098 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCCATTATG GATGGATGGG CGGGCTACG GCGTTGGCAC CAGTCTCTAG AAAAGAAGTC	60
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ACCTAGTGTGTT GCGGGGCAAA AAGGGTCTTG CCGGCCTCGC TGTGCAGGG GCGTATCTGG	180
GCGCCTGAGC GCGGCCTGGG AGCTTGGCA GCCGCCGAG CAGGGGGCAC ACCCGGAACC	240
GGCCTGAGCG CCCGGGACCA TGAACGGGGA GGCCATCTGC AGCGCCCTGC CCACCATTCC	300
CTACCACAAA CTCGCCGACC TGCGCTACCT GAGCCGCGGC GCCTCTGGCA CTGTGTCGTC	360
CGCCCGCCAC GCAGACTGGC GCCTCCAGGT GGCCGTGAAG CACCTGCACA TCCACACTCC	420
GCTGCTCGAC AGTGAAAGAA AGGATGTTTT AAGAGAAGCT GAAATTAC ACAAAAGCTAG	480
ATTTAGTTAC ATTTTCCAA TTTTGGGAAT TTGCAATGAG CCTGAATTGTT TGGGAATAGT	540
TACTGAATAC ATGCCAAATG GATCATTAAA TGAACCTCTA CATAGGAAAA CTGAATATCC	600
TGATGTTGCT TGGCCATTGA GATTCGCAT CCTGCATGAA ATTGCCCTTG GTGTAAATTA	660
CCTGCACAAT ATGACTCCTC CTTTACTTCA TCATGACTTG AAGACTCAGA ATATCTTATT	720
GGACAATGAA TTTCATGTTA AGATTGCAGA TTTTGGTTTA TCAAAGTGGC GCATGATGTC	780
CCTCTCACAG TCACGAAGTA GCAAATCTGC ACCAGAAGGA GGGACAATTA TTTATATGCC	840
ACCTGAAAAC TATGAACTG GACAAAAATC AAGGGCCAGT ATCAAGCACG ATATATATAG	900
CTATGCAGTT ATCACATGGG AAGTGTATC CAGAAAACAG CCTTTGAAG ATGTCACCAA	960
TCCTTGCAG ATAATGTATA GTGTGTCACA GAAGCATCGA CCTGTTATTA ATGAAGAAAG	1020
TTTGCATAT GATATACTC ACCGAGCACG TATGATCTCT CTAATAGAAA GTGGATGGGC	1080
ACAAAATCCA GATGAAAGAC CATCTTCTT AAAATGTTTA ATAGAACCTG AACCAAGTTT	1140
GAGAACATTT GAAGAGATAA CTTTCTTGA AGCTGTTATT CAGCTAAAGA AAACAAAGTT	1200
ACAGAGTGTGTT TCAAGTGCCA TTCACCTATG TGACAAGAAG AAAATGGAAT TATCTCTGAA	1260
CATACCTGTA AATCATGGTC CACAAGAGGA ATCATGTGGA TCCTCTCAGC TCCATGAAAA	1320
TAGTGGTTCT CCTGAAACTT CAAGGTCCT GCCAGCTCCT CAAGACAATG ATTTTTATC	1380
TAGAAAAGCT CAAGACTGTT ATTTTATGAA GCTGCATCAC TGTCCTGGAA ATCACAGTTG	1440
GGATAGCACC ATTCTGGAT CTCAAAGGGC TGCATTCTGT GATCACAAGA CCACTCCATG	1500
CTCTTCAGCA ATAATAAAATC CACTCTCAAC TGCAGGAAAC TCAGAACGTC TGCAGCCTGG	1560
TATAGCCCAG CAGTGGATCC AGAGCAAAAG GGAAGACATT GTGAACCAAA TGACAGAAGC	1620
CTGCCTTAAC CAGTCGCTAG ATGCCCTCT GTCCAGGGAC TTGATCATGA AAGAGGACTA	1680

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TGACATCCAA GGAGAAGAAT TTGCCAAAGT TATAGTACAA AAATTGAAAG ATAACAAACA 1800
AATGGGTCTT CAGCCTTACC CGGAAATACT TGTGGTTCT AGATCACCAT CTTAAATT 1860 ;
ACTTCAAAAT AAAAGCATGT AAGTGACTGT TTTTCAAGAA GAAATGTGTT TCATAAAAGG 1920
ATATTTATAT CTCTGTTGCT TTGACTTTT TTATATAAAA TCCGTGAGTA TTAAAGCTT 1980
AWWRAARGKT CTTTSRKTAATATTAGTCT CCCTCCATGA CACTGCAGTA TTTTTTTAA 2040
TTAATACAAG TAAAAAGTTG AATTTGAAAAA AAAAAAAAAA AAAAAAAA AAAAAAA 2098